

SUPPLEMENTARY MATERIAL

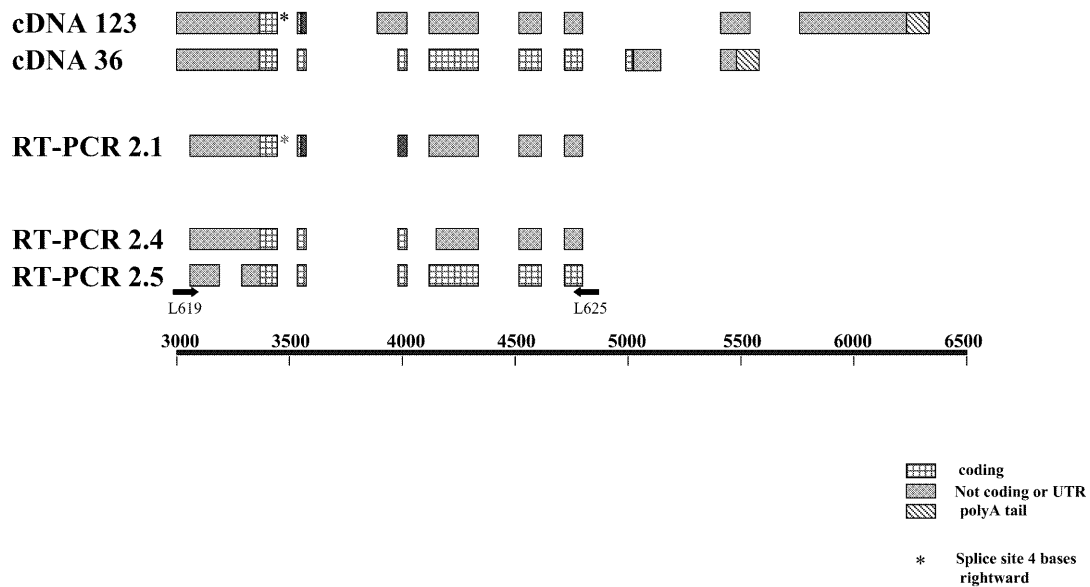


Figure S1.



Figure S2. (A) Sequence alignment for the first half of human MAD2B and ORF2 of *P.berghei*. By BLAST analysis the human protein showed the highest homology to ORF2 of *P.berghei*: score 51.9, *E* value $5e - 06$, identity 21%, similarity 45%. Boxed in black, sequence identity; boxed in grey, sequence similarity. (B) Sequence alignment for the first half of MAD-like proteins of nine different species including ORF2 of *P.berghei* and *P.falciparum*. The proteins vary in size between 185 and 211 amino acid residues. The sequence alignment of the second half of the MAD-like proteins is not significant, due to sequence divergence between the different subgroups of MAD-like proteins. Sequence identity and similarity are boxed as in Figure 3A. The species shown by abbreviated names are: *Caenorhabditis elegans*, *Arabidopsis thaliana*, *Xenopus laevis*, *Schizosaccharomyces pombe*, *Mus musculus* and *Homo sapiens*.